Amendments to the Specification

Please replace paragraph [0096] with the following paragraph:

A number of computer algorithms have been described for identification of peptides in a larger protein that may satisfy the requirements of peptide binding motifs for specific MHC class I or MHC class II molecules. Because of the extensive polymorphism of MHC molecules, different peptides will often bind to different MHC molecules. Tables 1-3 list C35 peptides predicted to be MHC binding peptides using three different algorithms. Specifically, Tables 1 and 5 list C35 HLA Class I and II epitopes predicted using the rules found at the SYFPEITIII website ~~(wysiWvg://35/http:1/134.2.96.221 /scripts/hlaserver.dll/ EpPredict.htm)~~ and are based on the book "MHC Ligands and Peptide Motifs" by Rammensee, H. G., Bachmann, J. and Stevanovic, S. (Chapman & Hall, New York 1997). Table 2 lists predicted MHC binding peptides derived from the C35 sequence using the NIH BIMAS program available on the web ~~(http://bimas.dcrt.nih.gzov/cgi-bin/molbio/ken parker comboform)~~. Finally, Tables 3 and 6 list predicted C35 peptides identified by the Tepitope program, a program for prediction of peptides that may bind to multiple different MHC class II molecules. Using Tepitope, four C35 peptides were identified as likely candidates for binding to a variety of HLA class II molecules. These peptides are, in general, longer than those binding to HLA class I and more degenerate in terms of binding to multiple HLA class II molecules.